

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=19; hr=16; min=11; sec=22; ms=759;]

=====

Application No: 10540959 Version No: 2.0

Input Set:

Output Set:

Started: 2008-08-21 20:25:40.203
Finished: 2008-08-21 20:25:41.003
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 800 ms
Total Warnings: 7
Total Errors: 0
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)

SEQUENCE LISTING

<110> Rennert, Paul D.

<120> KIM-1 ANTAGONISTS AND USE TO MODULATE
IMMUNE SYSTEM

<130> 13751-0055US1

<140> 10540959

<141> 2006-04-04

<150> PCT/US2003/041294

<151> 2003-02-29

<150> US 60/436,934

<151> 2002-12-30

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 359

<212> PRT

<213> Homo sapiens

<400> 1

Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp
1				5					10					15	
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val
			20					25					30		
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn
			35				40					45			
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr
	50					55				60					
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu
65				70					75					80	
Gly	Asp	Leu	Ser	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala	
			85					90				95			
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp
			100					105				110			
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
	115					120					125				
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130					135				140					
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr	
145				150					155					160	
Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr
			165					170				175			
Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro
			180					185				190			
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Thr	Val	Ser	Thr	Phe	Val	Pro
	195					200					205				
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro

210	215	220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala		
225	230	235
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp		240
	245	250
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn		255
	260	265
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr		270
	275	280
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala		285
	290	295
Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val		300
305	310	315
Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln		320
	325	330
Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu		335
	340	345
Asn Ser Leu Tyr Ala Thr Asp		350
	355	

<210> 2
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 2

Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp		
1	5	10
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val		
	20	25
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn		30
	35	40
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr		45
50	55	60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu		
65	70	75
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala		
	85	90
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp		95
	100	105
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys		110
	115	120
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val		125
	130	135
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr		140
145	150	155
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr		
	165	170
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro		175
	180	185
Thr Thr Thr Ser Val Pro Val Thr Thr Thr Val Ser Thr Phe Val Pro		190
	195	200
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro		205
	210	215
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala		220
225	230	235
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp		240

Lys Gly Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 290 295 300
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 305 310 315 320
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 325 330 335
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 340 345 350
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 355 360 365
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 370 375 380
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 385 390 395 400
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 405 410 415
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 420 425 430
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 435 440 445
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 450 455 460
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 465 470 475 480
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 485 490 495
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 500 505 510
 Ser Leu Ser Pro Gly Lys
 515

<210> 4

<211> 357

<212> PRT

<213> Artificial Sequence

<220>

<223> Human KIM-1 Partial Extracellular Domain Fc Construct

<400> 4

Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
 115 120 125

Val	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
130						135					140				
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
145					150					155					160
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
				165					170					175	
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
			180					185					190		
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
		195					200					205			
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
	210					215					220				
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
225					230					235					240
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
				245					250					255	
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln
			260					265					270		
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
		275					280					285			
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
	290					295					300				
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
305					310					315					320
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
				325					330					335	
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
			340					345					350		
Leu	Ser	Pro	Gly	Lys											
			355												

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal peptide for Human KIM-1 Extracellular
Domain Histag Construct

<400> 5

Val	Glu	His	His	His	His	His
1				5		

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 6

Asp	Tyr	Lys	Asp	Asp	Asp	Lys
1				5		

<210> 7

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Human KIM-1 Extracellular Domain Histag Construct

<400> 7

```
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1          5          10          15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr
145          150          155          160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr
165          170          175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
180          185          190
Thr Thr Thr Ser Val Pro Val Thr Thr Thr Val Ser Thr Phe Val Pro
195          200          205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
210          215          220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
225          230          235          240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
245          250          255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
260          265          270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
275          280          285
Lys Gly Val Glu His His His His His His
290          295
```

<210> 8

<211> 1398

<212> DNA

<213> Artificial Sequence

<220>

<223> Human KIM-1 Extracellular Domain Fe Construct Fc

<400> 8

atgaatcaga ttcaagtctt catttcaggc ctcatactgc ttctcccagg cactgtggat

tcttatgttg	aagtaaaagg	ggtagtggg	cacctgtca	cacttccatg	tacttactca	120
acatatcgtg	gaatcacaa	gacatgttg	ggccgaggg	aatgccatc	ttctgcttgt	180
caaaatacac	ttatttggac	caatggacat	cgtgtcacct	atcagaagag	cagtcggtac	240
aacttaaagg	ggcatatttc	agaaggagat	gtgtccttga	cgatagagaa	ctctgttgag	300
agtgacagtg	gtctgtattg	ttgtcagtg	gagattcctg	gatggtttaa	tgatcagaaa	360
gtgacctttt	cattgcaagt	taaaccagag	attcccacac	gtcctccaac	aagaccaca	420
actacaaggc	ccacagctac	aggaagaccc	acgactat	caacaagatc	cacacatgta	480
ccaacatcaa	tcagagtctc	tacctccact	cctccaacat	ctacacacac	atggactcac	540
aaaccagaac	ccactacatt	ttgtcccat	gagacaacag	ctgaggtgac	aggaatccca	600
tcccatactc	ctacagactg	gaatggcact	gcgacatcct	caggagatac	ctggagtaat	660
cacactgaag	caatccctcc	aggggaagccg	cagaaaaacc	ctactaaggg	cgctcgacaaa	720
actcacacat	gcccaccgtg	cccagcacct	gaactcctgg	ggggaccgtc	agtcttcctc	780
ttccccccaa	aaccaagga	caccctcatg	atctcccgga	cccctgaggt	cacatgcgtg	840
gtggtggacg	tgagccacga	agacctgag	gtcaagttca	actggtacgt	ggacggcgtg	900
gaggtgcata	atgccaagac	aaagccgcgg	gaggagcagt	acaacagcac	gtaccgtgtg	960
gtcagcgtcc	tcaccgtcct	gcaccaggac	tggctgaatg	gcaaggagta	caagtgcaag	1020
gtctccaaca	aagccctccc	agccccatc	gagaaaacca	tctccaaagc	caaagggcag	1080
ccccgagaac	cacaggtgta	caccctgcc	ccatccggg	atgagctgac	caagaaccag	1140
gtcagcctga	cctgctgg	caaaggcttc	tatccagcg	acatcgccgt	ggagtgggag	1200
agcaatgggc	agccggagaa	caactacaag	accacgcctc	ccgtgttgga	ctccgacggc	1260
tccttcttcc	tctacagcaa	gctcaccgtg	gacaagagca	ggtggcagca	ggggaacgtc	1320
ttctcatgct	ccgtgatgca	tgaggctctg	cacaaccact	acacgcagaa	gagcctctcc	1380
ctgtctcccg	ggaaatga					1398